

Amendments to the Specification

Please amend paragraphs [0065], and [0178] as follows:

[0065] FIG. 15 shows an alignment between the SARS virus Small envelope protein E (TOR2_E; SEQ ID NO: 35) and the Envelope protein (Protein 4) (X1 protein) (ORF 3) from Porcine transmissible gastroenteritis coronavirus (strain Purdue). Swissprot accession number P09048 (PGV; SEQ ID NO: 63), as calculated by FASTA (~~<http://www.ebi.ac.uk/fasta33/>~~) (world wide web at ebi "dot" ac "dot" uk "forward slash" fasta33).

[0178] The sequence information was imported into an ACEDB database (Durbin, J. Thierry-Mieg. 1991. A C. elegans Database. Documentation, code and data available from anonymous FTP servers at ~~lirmm.lirmm.fr~~, ~~cele.mrc-lmb.cam.ac.uk~~ and ~~ncbi.nlm.nih.gov~~ [lirmm "dot" lirmm "dot" fr](http://lirmm.lirmm.fr); [cele "dot" mrc-lmb "dot" cam "dot" ac "dot" uk](http://cele.mrc-lmb.cam.ac.uk); and [ncbi "dot" nlm "dot" nih "dot" gov](http://ncbi.nlm.nih.gov)) and subjected to biological analysis including the identification of open reading frames, detection of similar sequences by BLAST and searching for apparent frameshifts. When frameshifts were identified by this analysis, the sequence assembly was consulted for evidence of sequencing errors and if found, they were corrected. The sequences were also searched for any that could extend the 5' end of the sequence and these were incorporated when found. High quality sequence discrepancies between different sequence reads were identified and resolved. Sequence reads classified as deleted or chimeric were identified through manual inspection and removed from the assembly. The resulting sequence has an average PHRED consensus quality score of 89.96. The lowest quality bases in the assembly are in the immediate vicinity of the 5' and 3' ends of the viral genome, with the lowest quality base having a PHRED score of 35. Most (29,694 of the 29,736 (99.86%)) of the bases have a consensus score of 90. Almost all regions of the genome are represented by reads derived from both strands of the plasmid sequencing templates, the exceptions being 50 bases at the 5' end represented by a single sequencing read, and 5 bases at the 3' end represented by a single read. The average base in the assembly is represented by 30 reads in the forward direction and 30 reads in the reverse direction, as determined by PHRED. RT-PCR products predicted from the sequence and spanning the entire genome yield PCR products of the anticipated size on agarose gels. To confirm the 5' end of the viral genome RACE was performed using the RLM-RACE kit from Ambion, and primers 5'-CAGGAAACAGCTATGACACCAAGAACAAGGCTCTCCA-3' (SEQ ID NO: 90) and 5'-CAGGAAACAGCTATGACGATAGGGCCTCTTCCACAGA-3' (SEQ ID NO: 91). Fourteen clones

Application No.: 10/555,073
Office Action mailed October 28, 2009
Amendment filed April 28, 2010
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were recovered and sequenced. Analysis of these sequences confirmed the 5' end of the coronavirus genome. The SARS genomic sequences have been deposited into Genbank (Accession Nos. AY274119.1, AY274119.2, and AY274119.3).